



**COPY OF PAPERS
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SEQUENCE LISTING

<110> Merck & Co., Inc.
University of British Columbia

<120> APOPTOSIS MODULATORS THAT INTERACT WITH THE HUNTINGTON'S DISEASE GENE

130 MC010BT

<140> 09/701,205
<141> 2000-11-27

<150> PCT/US99/11743
<151> 1999-05-27

<150> 09/085,199
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Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys	Glu Lys	His Ser Glu				
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Leu Val His Val His Ala Glu Leu Leu Arg Lys	Asn Ala	Asp Thr Ala				
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Lys Gln Leu Thr Val Thr Gln Gln Ser Gln	Glu Val	Ala Arg Val				
85	90	95				
Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val	Lys Arg	Glu Ser Glu				
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Leu Lys Leu Glu Lys Ser Asp Gln Gln Glu Lys	Leu Lys	Arg Glu				
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 His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
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 Asp Leu Leu Ala Ala Glu Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
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 Arg Cys Thr Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
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 Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
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 565 570 575
 Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
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 Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
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 610 615 620

Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
 625 630 635 640
 Val Thr Thr Lys Lys Pro Pro Leu Ala Gln Lys Pro Ser Val Ala Pro
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Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys	35	40	45
Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn	50	55	60
Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn	65	70	75
Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile	85	90	95
Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn	100	105	110
Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val	115	120	125
Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln	130	135	140
Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys	145	150	155
Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile	165	170	175
Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu	180	185	190
Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn	195	200	205
Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp	210	215	220
Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser	225	230	235
Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Asp Val Leu Glu Asn	245	250	255
Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His	260	265	270
Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln	275	280	285
Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala	290	295	300
Gln Arg Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr	305	310	315
Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Val Leu	325	330	335
Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg	340	345	350
Glu Ile Gln Glu Ala Leu Ser Gln Glu Leu Glu Pro Thr Leu Ile Ser	355	360	365
Cys Ala Gly Ser Thr Asp His Leu Leu Ser Lys Val Ser Ser Val Ser	370	375	380
Ser Cys Leu Glu Gln Leu Glu Lys Asn Gly Ser Gln Tyr Leu Ala Cys	385	390	395
Pro Glu Asp Ile Ser Glu Leu Leu His Ser Ile Thr Leu Leu Ala His	405	410	415
Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala	420	425	430
Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly	435	440	445
Arg Glu Thr Leu Ala Tyr Leu Ser Ser Leu Glu Glu Gly Thr Val	450	455	460
Glu Asn Ala Asp Val Thr Ala Leu Arg Asn Cys Leu Ser Arg Val Lys	465	470	475
Thr Leu Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu	485	490	495
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 675 680 685
 Ser Met Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val
 690 695 700
 Arg Val Leu Glu Leu Glu Asn Asp Leu Gln Lys Glu Arg Gln Lys Leu
 705 710 715 720
 Gly Glu Leu Arg Lys His Tyr Glu Leu Glu Gly Val Ala Glu Gly
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 Lys His Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
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 Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
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Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
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 Gly His Pro Asn Val Leu His Asp Tyr Glu Arg Tyr Arg Ser Asn Ile
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 Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
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 Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
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 Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
 180 185 190
 Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
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 Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
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 His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
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 245 250 255
 Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
 260 265 270
 Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
 275 280 285
 Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
 290 295 300
 Ile Pro Glu Glu Ala Pro Glu Glu Glu Pro Glu Asn Leu Ile Glu
 305 310 315 320
 Ile Ser Ser Ala Pro Pro Ala Gly Glu Pro Val Val Val Ala Asp Leu
 325 330 335
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